PATENT CLAIMS

1. Plant DNA-sequence:

ACTTTTCGAG CCCCTTGAAC TGGAAATTAA TACATTTTCC ACTTGACTTT TGAAAAGGAG GCAATCCCAC GGGAGGGAAG CTGCTACCAA CCTTCGTAAT GTTAATGAAA TCAAAGTCAC TCAATGTCCG AATTTCAAAC CTCANCAACC CAATAGCCAA T.

2. DNA sequence, as set forth in Claim 1, which originates from grapevine (Vitis vinifera).

3. DNA sequence, as set forth in Claims 1 or 2, which is naturally contained in the stilbene-synthase gene, Vstl, and corresponds to base pairs -270 to -430.

4. Promotor region of the stilbene-synthase gene, Vstl, from grapevine, which lacks at least the DNA sequence, as set forth in Claim 1.

5. Promotor region, as set forth in Claim 4, which comprises only the sequence range from the start of the translation up to base pair -270.

6. Promotor region, as set forth in Claims 4 or 5, which still conveys a pathogen-induced gene expression in plant cells.

7. Chimeric nucleic-acid molecules into which the DNA-sequence, as set forth in Claim No. 1, or at least a fragment thereof has been introduced.

8. Chimeric nucleic-acid molecules, as set forth in Claim No. 7, which render possible in plants an ozone-inducible expression of the coding regions contained in said molecules.

9. Vectors which contain the DNA sequence, a promotor region or a chimeric nucleic-acid molecule, as set forth in one of the preceding claims, or fragments thereof.

10. Transgenic plants which contain the DNA sequence, a promotor region or a chimeric nucleic-acid molecule, as set forth in one of the preceding claims, or a DNA sequence derived from said DNA sequence, as well as constituents of such plants and their propagating material such as protoplasts, plant cells, calli, seeds, tubers or cuttings, etc. as well as the offsprings of such plants.

11. Transgenic plants which, due to the absence (present in the natural state) DNA sequence ACTTTTCGAG CCCCTTGAAC TGGAAATTAA TACATTTTCC ACTTGACTTT TGAAAAGGAG GCAATCCCAC GGGAGGGAAG CTGCTACCAA CCTTCGTAAT GTTAATGAAA TCAAAGTCAC TCAATGTCCG AATTTCAAAC CTCANCAACC CAATAGCCAA T
or due to the lack of at least one fragment thereof no longer show an ozone-inducible expression of the naturally ozone-inducible gene.

12. Plants, as set forth in Claim 11, in which the ozone-inducible expression of disease-resistant genes is greatly reduced.

13. Plants, as set forth in Claims 11 or 12 in which the ozone-inducible expression of stilbene-synthase genes, particularly that of the Vstl gene from grapevine, is greatly reduced.

14. Plants, as set forth in Claim 10, in which, due to the introduction of the DNA sequence, as set forth in Claim No. 1, or at least a fragment thereof, an ozone-inducible gene expression of a gene in which said DNA sequence does not naturally occur, can take place.

15. Plants, as set forth in Claim 14, in which an ozone-inducible expression of those genes can take place, whose gene products in plant cells are able to detoxify reactive oxygen species.

16. Plants, as set forth in Claims 14 or 15, in which an ozone-inducible expression of catalase or superoxide-dismutase genes can take place.

17. Plants, as set forth in Claim No. 14, in which an ozone-inducible expression of reporter genes can occur.

18. Dicotyle plants, as set forth in one of Claims 10 to 17, in particular useful plants, such as soya bean, rape, tomato, sugar beet, potato, cotton, tobacco, as well as ornamental plants or trees.

19. Monocotyle plants, as set forth in one of Claims 10 to 17, especially grain such as oat, wheat, rye, barley, rice, millet or corn.

20. Transgenic plant cells, including protoplasts, which contain the DNA sequence, a promoter region or a chimeric nucleic-acid molecule, as set forth in one of Claims 1 to 9, or a DNA sequence derived therefrom.

21. Plant cells, including protoplasts, which, due to the absence (present in the natural state) of the DNA sequence

ACTTTTCGAG CCCCTTGAAC TGGAAATTAA TACATTTTCC ACTTGACTTT TGAAAAGGAG GCAATCCCAC GGGAGGGAAG CTGCTACCAA CCTTCGTAAT GTTAATGAAA TCAAAGTCAC TCAATGTCCG AATTTCAAAC CTCANCAACC CAATAGCCAA T,

or due to lack of at least one fragment thereof, no longer show an ozone-inducible expression of the naturally ozone-inducible gene.

22. Plant cells, as set forth in Claim 20, in which, due to the introduction of the DNA sequence, as set forth in Claim 1, or at least a fragment thereof, an ozone-inducible gene expression of a gene in which said DNA sequence does not naturally occur, can take place.

23. Methods for producing transgenic plants or plant cells in which the ozone-inducible expression of naturally ozone-inducible, defensive genes are greatly reduced or eliminated by deleting the DNA sequence, as set forth in Claim No. 1, or at least a fragment thereof in the defensive gene which naturally contains said DNA sequence or a DNA sequence derived therefrom.

24. Processes, as set forth in Claim 23, in which the ozone-inducible expression of stilbene-synthase genes will be greatly reduced or eliminated.

25. Processes, as set forth in Claims Nos. 23 or 24, in which the ozone-inducible expression of the VstI gene from grapevine will be greatly reduced or eliminated.

26. Methods for the production of transgenic plants or plant cells in which one or several genes - the expression thereof is not naturally or not substantially induced through ozone - are ozone inducible due to the introduction of the DNA-sequence, as set forth in Claim 1, or at least a fragment thereof.

27. Methods, as set forth in Claim 26, in which one or several catalase and/or superoxide-dismutase genes are induced through ozone.

28. Processes, as set forth in Claim 26, in which one or several reporter genes are inducible through ozone.

29. Methods to remove the ozone inducibility of naturally ozone-inducible defensive genes which naturally contain the DNA-sequence, as set forth in Claim 1, or a DNA sequence derived therefrom, through the deletion or inactivation of the DNA sequence, as set forth in Claim 1, or at least a fragment thereof.

30. A process, as set forth in Claim 29, in which the gene is a stilbene-synthase gene.

31. A process, as set forth in Claims 29 or 30 in which the gene is the Vstl gene from grapevine.

32. A method for producing ozone-inducible characteristics in transgenic plants or plant cells by inserting the DNA sequence, according to Claim 1, or at least a fragment thereof, into those genes which are not naturally or not substantially inducible through ozone.

33. The use of the DNA sequence, as set forth in Claim 1, or a fragment thereof for detecting ozone-responsive sequence ranges in genes of plants.

34. The use of the DNA sequence, as set forth in Claim 1, or a fragment thereof to produce ozone-inducible characteristics in transgenic plants or plant cells.

35. The use of the DNA sequence, as set forth in Claim 1, or a fragment thereof, to produce plants, according to Claim 17, which can be used as biomonitors for the quantitative and/or qualitative determination of ozone concentrations.

36. The use of the promoter region, as set forth in one of Claims 4 to 6, to produce greater pathogen-inducible but not ozone-inducible resistance to disease in transgenic plants.

Illustration 1

(b) Replacement Sheet (Rule 26)

(a) GUS activity [pmol MU min^{-1} mg^{-1} protein]

(b) 100 nL L^{-1} ozone
Control
200 nL L^{-1} ozone
Control
400 nL L^{-1} ozone
Control

(c) Ozone gassing

(d) Time (h)

(e) Illustration 2

(f) Replacement Sheet (Rule 26)